

GenCore version 4.5
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OM protein - protein search, using SW model

Run on: March 15, 2002, 06:26:26 ; Search time 188.13 Seconds
(without alignments)
59.035 Million cell updates/sec

Title: US-09-856-050-19
Perfect score: 220
Sequence: 1 MNLILTFVAANAARFDDDKLVHGKLNHHNHHDDDK 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues 3148936
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

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3:	/cgn2_6/ptodata/2/paa/US07_COMB.pep:*
4:	/cgn2_6/ptodata/2/paa/US08_COMB.pep:*
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23:	/cgn2_6/ptodata/2/paa/US099_COMB.pep:*
24:	/cgn2_6/ptodata/2/paa/US060_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	220	100.0	40	22	US-09-856-050-19
2	122	55.5	247	23	US-09-923-779-154
3	122	55.5	247	24	US-60-230-435-1545
4	112	50.9	247	1	PCR-US00-28558-4
5	112	50.9	247	18	US-09-418-527C-4
6	112	50.9	280	24	US-60-212-659-307
7	112	50.9	280	24	US-60-230-435-1884
8	110	50.0	251	21	US-09-760-475-2344
9	104	47.3	180	24	US-60-213-800-342

10	102	46.4	247	24	US-60-212-659-308	Sequence 308, App
11	102	46.4	247	24	US-60-230-435-1885	Sequence 1885, Ap
12	98	44.5	247	21	US-09-760-475-2359	Sequence 2359, Ap
13	91	41.4	247	21	US-09-762-277-1	Sequence 1, Appl
14	90	40.9	53	20	US-09-605-784A-1262	Sequence 1262, Ap
15	86	39.1	45	22	US-09-856-050-17	Sequence 17, Appl
16	84	38.2	281	8	US-08-467-155-7	Sequence 7, Appl
17	81	36.8	246	13	US-08-978-404A-44	Sequence 44, Appl
18	79	35.9	20	20	US-09-674-677-34	Sequence 34, Appl
19	77	35.0	183	10	US-08-691-274-9	Sequence 9, Appl
20	76	34.5	76	22	US-09-869-446-2	Sequence 2, Appl
21	76	34.5	124	22	US-09-869-446-9	Sequence 9, Appl
22	75.5	34.3	401	19	US-09-538-092-572	Sequence 572, App
23	75	34.1	51	1	PCR-US00-05989-566	Sequence 566, App
24	75	34.1	51	23	US-09-925-297-566	Sequence 566, App
25	74	33.6	284	1	PCR-US00-22271-54	Sequence 54, Appl
26	74	33.6	284	1	PCR-US00-22283-54	Sequence 54, Appl
27	74	33.6	284	17	US-09-386-642-54	Sequence 54, Appl
28	74	33.6	288	1	PCR-US00-09973-13	Sequence 13, Appl
29	74	33.6	288	1	PCR-US00-22271-13	Sequence 13, Appl
30	74	33.6	288	1	PCR-US00-22283-13	Sequence 13, Appl
31	74	33.6	288	17	US-09-303-162-13	Sequence 13, Appl
32	74	33.6	288	17	US-09-386-642-13	Sequence 13, Appl
33	74	33.6	289	1	PCR-US00-09973-14	Sequence 14, Appl
34	74	33.6	289	1	PCR-US00-22271-14	Sequence 14, Appl
35	74	33.6	289	1	PCR-US00-22283-14	Sequence 14, Appl
36	74	33.6	289	17	US-09-303-162-14	Sequence 14, Appl
37	74	33.6	289	17	US-09-386-642-14	Sequence 14, Appl
38	74	33.6	292	1	PCR-US01-18568-9	Sequence 9, Appl
39	74	33.6	292	1	PCR-US01-18568A-9	Sequence 9, Appl
40	74	33.6	315	1	PCR-US00-23823-9	Sequence 9, Appl
41	74	33.6	315	17	US-09-386-653-9	Sequence 9, Appl
42	74	33.6	315	17	US-09-386-653A-9	Sequence 9, Appl
43	74	33.6	316	17	US-09-387-375-9	Sequence 9, Appl
44	74	33.6	327	17	US-09-386-659-8	Sequence 8, Appl
45	74	33.6	328	1	PCR-US00-09973-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-856-050-19
Sequence 19, Application US/09856050
GENERAL INFORMATION:
APPLICANT: UEMURA, Hidetoshi
APPLICANT: OKUI, Akira
APPLICANT: KOMINAMI, Katsuya
APPLICANT: YAMAGUCHI, Nozomi
APPLICANT: MITSUI, Shinichi
TITLE OF INVENTION: PROTEIN EXPRESSION VECTOR AND USE THEREOF
FILE REFERENCE: UEMURA-8
CURRENT APPLICATION NUMBER: US/09/856, 050
CURRENT FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: JP 10/331515
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/JP99/06474
PRIOR FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 40
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Synthetic
US-09-856-050-19

Query Match 100.0% Score 220; DB 22; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

;; TITLE OF INVENTION: Extracellular Serine Protease and Uses Thereof

US-60-212-659-307


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; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: C1000768
; CURRENT APPLICATION NUMBER: US/60/230,435
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 2991
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1885
; LENGTH: 247
; TYPE: PRN
; ORGANISM: HUMAN
US-60-230-435-1885

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Query Match          46.4%; Score 102; DB 24; Length 247;
Best Local Similarity 77.8%; Pred. No. 0.00011;
Matches 21; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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OY 1 MNLILITFVAAVAAPFDDDDKLVHG 27
Db 1 MNPILLIAFVGAAVAVPDDDDKIVG 27

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```

RESULT 12
US-09-760-475-2359
; Sequence 2359, Application US/09760475
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antbodies
; FILE REFERENCE: PTZ49
; CURRENT APPLICATION NUMBER: US/09/760,475
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2359
; LENGTH: 247
; TYPE: PRN
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (62)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (79)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-760-475-2359

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Query Match          44.5%; Score 98; DB 21; Length 247;
Best Local Similarity 74.1%; Pred. No. 0.00036;
Matches 20; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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OY 1 MNLILITFVAAVAAPFDDDDKLVHG 27
Db 1 MNPILLIAFVGAAVAVPDDDDKIVG 27

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```

RESULT 13
US-09-762-277-1
; Sequence 1, Application US/09762277
; GENERAL INFORMATION:
; APPLICANT: Fuji Yakuhin Kogyo Kabushiki Kaisha
; TITLE OF INVENTION: Monoclonal Antibody against Canine Trypsin
; FILE REFERENCE: FJ-94PCT
; CURRENT APPLICATION NUMBER: US/09/762,277
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: JP 10-236609
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: JP 11-63990
; PRIOR FILING DATE: 1999-03-10

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```

; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 247
; TYPE: PRN
; ORGANISM: Dog Pancreas
US-09-762-277-1

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```

Query Match          41.4%; Score 91; DB 21; Length 247;
Best Local Similarity 70.4%; Pred. No. 0.0028;
Matches 19; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

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OY 1 MNLILITFVAAVAAPFDDDDKLVHG 27
Db 1 MNPILLIAFVGAAVAVPDDDDKIVG 27

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```

RESULT 14
US-09-605-784A-1262
; Sequence 1262, Application US/09605784A
; GENERAL INFORMATION:
; APPLICANT: Sharp, John D.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND ENCODED
; FILE REFERENCE: 1600.1138-001
; CURRENT APPLICATION NUMBER: US/09/605,784A
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/141,228
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 2322
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1262
; LENGTH: 53
; TYPE: PRN
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(53)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-605-784A-1262

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Query Match          40.9%; Score 90; DB 20; Length 53;
Best Local Similarity 74.1%; Pred. No. 0.00073;
Matches 20; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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OY 1 MNLILITFVAAVAAPFDDDDKLVHG 27
Db 1 MNPILLIAFVGAAVAVPDDDDKIVG 27

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RESULT 15
US-09-856-050-17
; Sequence 17, Application US/09856050
; GENERAL INFORMATION:
; APPLICANT: UEMURA, Hidetoshi
; APPLICANT: OKUI, Akira
; APPLICANT: KOMINAMI, Katsuya
; APPLICANT: YAMAGUCHI, Nozomi
; APPLICANT: MITSUI, Shinichi
; TITLE OF INVENTION: PROTEIN EXPRESSION VECTOR AND USE THEREOF
; FILE REFERENCE: UEMURA=8
; CURRENT APPLICATION NUMBER: US/09/856,050
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: JP 10/331515
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCT/JP99/06474
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 45

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-856-050-17
    
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Query Match          39.1%; Score 86; DB 22; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 KLHHHHHDDDDK 40
DB 33 KLHHHHHDDDDK 45
    
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Search completed: March 15, 2002, 06:48:48
 Job time: 1342 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 15, 2002, 06:26:26 ; Search time 17.14 Seconds

(without alignments)
148.848 Million cell updates/sec

Title: US-09-856-050-19
Perfect score: 220
Sequence: 1 MNLLILTFVAAVAAPFDDDDKLVHGKLNHHHHDDDK 40

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 302707 seqs, 63781257 residues

Total number of hits satisfying chosen parameters: 302707

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
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4: /cgn2_6/ptodata/1/paa/US08_NEM_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEM_COMB.pep:*
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7: /cgn2_6/ptodata/1/paa/US10_NEM_COMB.pep:*
8: /cgn2_6/ptodata/1/paa/US60_NEM_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	50.9	247	6	US-09-907-187A-4
2	91	41.4	247	6	US-09-762-277A-1
3	84	38.2	246	6	US-09-831-180A-53
4	84	38.2	246	6	US-09-842-758-55
5	84	38.2	281	7	US-10-021-368-7
6	75.5	34.3	401	6	US-09-550-398C-104
7	75.5	34.3	401	6	US-09-911-882-20
8	75.5	34.3	401	6	US-09-911-882-20
9	75.5	34.3	401	6	US-09-911-927-20
10	74	33.6	198	6	US-09-708-427-49415
11	74	33.6	315	7	US-10-040-655-9
12	74	33.6	315	7	US-10-041-006-9
13	74	33.6	327	7	US-10-040-803-8
14	72	32.3	149	6	US-09-620-111B-5168
15	71	32.3	132	6	US-09-708-427-58802
16	69	31.4	85	6	US-09-620-111B-1590
17	69	31.4	90	6	US-09-620-111B-1589
18	69	31.4	94	6	US-09-620-111B-8431
19	69	31.4	106	6	US-09-620-111B-8431
20	69	31.4	111	6	US-09-620-111B-133
21	69	31.4	114	6	US-09-620-394B-8
22	69	31.4	114	6	US-09-620-111B-4893
23	69	31.4	119	6	US-09-620-111B-4892
24	69	31.4	121	6	US-09-620-111B-7542
25	69	31.4	126	6	US-09-620-111B-7541

26	69	31.4	134	6	US-09-620-111B-1588	Sequence 1588, Ap
27	69	31.4	151	6	US-09-620-111B-4891	Sequence 4891, Ap
28	69	31.4	155	6	US-09-620-111B-131	Sequence 131, App
29	69	31.4	156	6	US-09-620-111B-7540	Sequence 7540, Ap
30	68	30.9	195	6	US-09-284-101-4	Sequence 4, Appl
31	68	30.9	199	6	US-09-708-427-55401	Sequence 55401, A
32	68	30.9	231	6	US-09-708-427-55400	Sequence 55400, A
33	68	30.9	281	6	US-09-708-427-55399	Sequence 55399, A
34	67.5	30.7	127	6	US-09-481-620A-40	Sequence 40, Appl
35	67.5	30.7	127	6	US-09-481-620A-72	Sequence 72, Appl
36	67.5	30.7	131	6	US-09-708-427-82155	Sequence 82155, A
37	67.5	30.7	207	6	US-09-708-427-82154	Sequence 82154, A
38	67.5	30.7	218	6	US-09-708-427-82153	Sequence 82153, A
39	67	30.5	246	6	US-09-762-277A-2	Sequence 2, Appl
40	66.5	30.2	20	1	PCR-US01-44516-5	Sequence 5, Appl
41	66.5	30.2	24	6	US-09-613-972-22	Sequence 22, Appl
42	66.5	30.2	24	7	US-10-080-455-5	Sequence 5, Appl
43	66	30.0	23	6	US-09-939-126-7	Sequence 7, Appl
44	66	30.0	88	6	US-09-614-150-29439	Sequence 29439, A
45	66	30.0	109	6	US-09-380-913-33	Sequence 33, Appl

ALIGNMENTS

```

RESULT 1
US-09-907-187A-4
; Sequence 4, Application US/09907187A
; GENERAL INFORMATION:
; APPLICANT: Underwood, Lowell
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Shigemasa, Kazushi
; TITLE OF INVENTION: Tumor Antigen-Derived Gene 16 (TAG-16): A Novel
; FILE OF INVENTION: Extracellular Serine Protease and Uses Thereof
; FILE REFERENCE: D6250D
; CURRENT APPLICATION NUMBER: US/09/907,187A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 09/418,527
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 179
; SEQ ID NO 4
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; OTHER INFORMATION: Sequence of Trypsinogen
US-09-907-187A-4

Query Match          50.9%; Score 112; DB 6; Length 247;
Best Local Similarity 85.2%; Pred. No. 4.5e-08;
Matches 23; Conserved 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNLLILTFVAAVAAPFDDDDKLVHG 27
  |||||||:|:|:|:|:|:|:|:|:|:|:|
DB 1 MNPLILTFVAAALAPFDDDDKIVGG 27

RESULT 2
US-09-762-277A-1
; Sequence 1, Application US/09762277A
; GENERAL INFORMATION:
; APPLICANT: Fuji Yakuhin Kogyo Kabushiki Kaisha
; TITLE OF INVENTION: Monoclonal Antibody against Canine Trypsin
; FILE REFERENCE: FJ-94PCT
; CURRENT APPLICATION NUMBER: US/09/762,277A
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: JP 10-236609
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: JP 11-63990
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 5

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RESULT 4
US-09-842-758-55
: Sequence 55. Application US/09842758
: GENERAL INFORMATION:
: APPLICANT: Vernet, Corine A. M.
: APPLICANT: Fernandes, Elma R
: APPLICANT: Gerlach, Valerie
: APPLICANT: Shinkets, Richard A
: APPLICANT: Malvankar, Uriel M
: APPLICANT: Boldog, Ferenc L
: APPLICANT: Zernhusen, Bryan D
: APPLICANT: Spytek, Kimberly A
: APPLICANT: Majumder, Kumud
: APPLICANT: Tchernev, Velizar T
: APPLICANT: Padigar, Muralidhara
: APPLICANT: Patturajan, Meera
: APPLICANT: Burgess, Catherine E
: APPLICANT: Gangoli, Esha A
: APPLICANT: Smithson, Glenda
: APPLICANT: Rastelli, Luca
: APPLICANT: Macdougall, John R
: APPLICANT: Taupier, Raymond J
: APPLICANT: Grosse, William M
: APPLICANT: Edward, Szekeres S

RESULT 5
 US-10-021-368-7
 Sequence 7, Application US/10021368
 GENERAL INFORMATION:
 APPLICANT: Band, Vimla
 TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA, AND RELATED
 MOLECULES AND METHODS
 NUMBER OF SEQUENCE ADDRESSES: 11
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/021.368

FILING DATE: 12-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/201,038
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/100002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
MOLECULE TYPE: protein
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-021-368-7

Query Match 38.2%; Score 84; DB 7; Length 281;
Best Local Similarity 66.7%; Pred. No. 0.00044;
Matches 18; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 MNLITLTVAAVAAPDDDDKLVHG 27
I: ||||| ||||| ||||| ||||| |||||
DB 1 MSALLILALVGAAVAPVDDDDKIVGG 27

RESULT 6
US-09-550-398C-104
Sequence 104, Application US/09550398C
GENERAL INFORMATION:
APPLICANT: Kurnasov, Oleg
APPLICANT: Overbeek, Ross
APPLICANT: Shatalin, Konstantin
APPLICANT: Osterman, Andrei
TITLE OF INVENTION: Novel Nicotinamide Mononucleotide Adenyltransferases
FILE REFERENCE: 2002.0030000
CURRENT APPLICATION NUMBER: US/09/550,398C
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 154
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 104
LENGTH: 401
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-550-398C-104

Query Match 34.3%; Score 75.5; DB 6; Length 401;
Best Local Similarity 39.5%; Pred. No. 0.011;
Matches 15; Conservative 7; Mismatches 13; Indels 3; Gaps 1;

QY 6 ILTFVAAVAAPDDDDKLVHGKLNHHNH--DDDDK 40
I: ||||| ||||| ||||| ||||| |||||
DB 38 VLADANSSIDAPFNIRKKRKHPRHHHHSRKEGNDK 75

RESULT 7
US-09-911-882-20
Sequence 20, Application US/09911882
GENERAL INFORMATION:
APPLICANT: Koltin, Yigal
APPLICANT: Gavrias, Victoria
TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
FILE REFERENCE: 06286-062004
CURRENT APPLICATION NUMBER: US/09/911,882
CURRENT FILING DATE: 2001-07-23

PRIOR APPLICATION NUMBER: US 08/965,762
PRIOR FILING DATE: 1997-11-07
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 401
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-911-882-20

Query Match 34.3%; Score 75.5; DB 6; Length 401;
Best Local Similarity 39.5%; Pred. No. 0.011;
Matches 15; Conservative 7; Mismatches 13; Indels 3; Gaps 1;

QY 6 ILTFVAAVAAPDDDDKLVHGKLNHHNH--DDDDK 40
I: ||||| ||||| ||||| ||||| |||||
DB 38 VLADANSSIDAPFNIRKKRKHPRHHHHSRKEGNDK 75

RESULT 8
US-09-911-888-20
Sequence 20, Application US/09911888
GENERAL INFORMATION:
APPLICANT: Koltin, Yigal
APPLICANT: Gavrias, Victoria
TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
FILE REFERENCE: 06286-062002
CURRENT APPLICATION NUMBER: US/09/911,888
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 08/965,762
PRIOR FILING DATE: 1997-11-07
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 401
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-911-888-20

Query Match 34.3%; Score 75.5; DB 6; Length 401;
Best Local Similarity 39.5%; Pred. No. 0.011;
Matches 15; Conservative 7; Mismatches 13; Indels 3; Gaps 1;

QY 6 ILTFVAAVAAPDDDDKLVHGKLNHHNH--DDDDK 40
I: ||||| ||||| ||||| ||||| |||||
DB 38 VLADANSSIDAPFNIRKKRKHPRHHHHSRKEGNDK 75

RESULT 9
US-09-911-927-20
Sequence 20, Application US/09911927
GENERAL INFORMATION:
APPLICANT: Koltin, Yigal
APPLICANT: Gavrias, Victoria
TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
FILE REFERENCE: 06286-062003
CURRENT APPLICATION NUMBER: US/09/911,927
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 08/965,762
PRIOR FILING DATE: 1997-11-07
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 401
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-911-927-20

Query Match 34.3%; Score 75.5; DB 6; Length 401;
Best Local Similarity 39.5%; Pred. No. 0.011;

Matches 15; Conservative 7; Mismatches 13; Indels 3; Gaps 1;

QY 6 ILTFVAAPFDDDDKLVHGKLNHHNNH--DDDDK 40
DB 38 VLADANSSIDAPFNIRKKRKHNNHHHSRKEGNDK 75

RESULT 10
US-09-708-427-49415

; Sequence 49415, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1243P
; CURRENT APPLICATION NUMBER: US/09/708,427
; CURRENT FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 85364
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49415
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 1..198
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc-feature
; LOCATION: 1..198
; OTHER INFORMATION: Ceres Seq. ID 1921855
US-09-708-427-49415

Query Match 33.6%; Score 74; DB 6; Length 198;
Best Local Similarity 36.2%; Pred. No. 0.0072;
Matches 17; Conservative 6; Mismatches 16; Indels 8; Gaps 1;

QY 1 NLLILITFVAAPFDDDDKLVHGK-----LHHNNHDDDD 39
DB 6 VGVLLAVALFAAARADDDKTPMQCFRSCSGCHHHHDHNDN 52

RESULT 11
US-10-040-655-9
; Sequence 9, Application US/10040655
; GENERAL INFORMATION:
; APPLICANT: Andrade-Gordon, Patricia
; APPLICANT: Darrow, Andrew
; TITLE OF INVENTION: DNA encoding the novel human serine
; FILE REFERENCE: ORT-1032
; CURRENT APPLICATION NUMBER: US/10/040,655
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein
; OTHER INFORMATION: of Protease T in a zymogen activation construct
US-10-040-655-9

Query Match 33.6%; Score 74; DB 7; Length 315;
Best Local Similarity 52.8%; Pred. No. 0.013;
Matches 19; Conservative 2; Mismatches 5; Indels 10; Gaps 1;

QY 2 NLLILITFV-----AAVAAPFDDDDKLVHG 27
DB 20 NLLICGVSDYKDDDDVDAAALAAPFDDDDKIVGG 55

RESULT 12
US-10-041-006-9

; Sequence 9, Application US/10041006
; GENERAL INFORMATION:
; APPLICANT: Andrade-Gordon, Patricia
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jian-shen
; TITLE OF INVENTION: DNA encoding the novel human serine
; FILE REFERENCE: ORT-1032
; CURRENT APPLICATION NUMBER: US/10/041,006
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein
; OTHER INFORMATION: of Protease T in a zymogen activation construct
US-10-041-006-9

Query Match 33.6%; Score 74; DB 7; Length 315;
Best Local Similarity 52.8%; Pred. No. 0.013;
Matches 19; Conservative 2; Mismatches 5; Indels 10; Gaps 1;

QY 2 NLLILITFV-----AAVAAPFDDDDKLVHG 27
DB 20 NLLICGVSDYKDDDDVDAAALAAPFDDDDKIVGG 55

RESULT 13
US-10-040-803-8
; Sequence 8, Application US/10040803
; GENERAL INFORMATION:
; APPLICANT: Andrade-Gordon, Patricia
; APPLICANT: Darrow, Andrew L.
; TITLE OF INVENTION: DNA encoding human serine protease C-E
; FILE REFERENCE: ORT-1030
; CURRENT APPLICATION NUMBER: US/10/040,803
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C-E catalytic
; OTHER INFORMATION: domain fusion protein
US-10-040-803-8

Query Match 33.6%; Score 74; DB 7; Length 327;
Best Local Similarity 52.8%; Pred. No. 0.013;
Matches 19; Conservative 2; Mismatches 5; Indels 10; Gaps 1;

QY 2 NLLILITFV-----AAVAAPFDDDDKLVHG 27
DB 20 NLLICGVSDYKDDDDVDAAALAAPFDDDDKIVGG 55

RESULT 14
US-09-620-111B-5168
; Sequence 5168, Application US/09620111B
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid

```

; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 2750-1070P
; CURRENT APPLICATION NUMBER: US/09/620,11B
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 9298
; SEQ ID NO 5168
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..149
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: 1..149
; OTHER INFORMATION: Ceres Seq. ID 1332728
US-09-620-11B-5168

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Query Match          32.7%; Score 72; DB 6; Length 149;
Best Local Similarity 42.1%; Pred. No. 0.0096;
Matches 16; Conservative 3; Mismatches 11; Indels 8; Gaps 1;

```

```

QY 10 VAAVAAPEDDDKLVHGK-----LHHHHHHDDD 39
      ||| | ||| | : ||| | | |
DB 34 LAAATARAADDDDKTPWQCFKSCSRGCHHHHHDDHDN 71

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RESULT 15
US-09-708-427-58802
; Sequence 58802, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: THEREBY
; FILE REFERENCE: 2750-1243P
; CURRENT APPLICATION NUMBER: US/09/708,427
; CURRENT FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 85364
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58802
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..132
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: 1..132
; OTHER INFORMATION: Ceres Seq. ID 1942723
US-09-708-427-58802

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Query Match          32.3%; Score 71; DB 6; Length 132;
Best Local Similarity 78.6%; Pred. No. 0.011;
Matches 11; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
QY 26 HGKLIHHHHHHDDD 39
      || | ||| | | | |
DB 94 HG--HHHHHHHEDD 105

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Search completed: March 15, 2002, 06:45:32
 Job time: 1146 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 06:26:26 ; Search time 12.51 seconds
(without alignments)
71.953 Million cell updates/sec

Title: US-09-856-050-19

Perfect score: 220
Sequence: 1 MNLILITFVAAGAAVAFDDDKLVHGKLNHHHHDDDK 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
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4: /cgn2_6/prodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/Backfillsl1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	38.2	281	1 US-08-467-155A-7	Sequence 7, Appl
2	84	38.2	281	2 US-08-628-198-7	Sequence 7, Appl
3	84	38.2	281	4 US-09-201-038-7	Sequence 7, Appl
4	84	38.2	281	5 PCT-US96-07343-7	Sequence 7, Appl
5	81	36.8	246	2 US-08-978-404B-44	Sequence 44, Appl
6	75.5	34.3	401	4 US-08-965-762-20	Sequence 20, Appl
7	71	32.3	247	2 US-08-956-267A-2	Sequence 2, Appl
8	68	30.9	14	1 US-08-226-264-7	Sequence 2, Appl
9	68	30.9	14	1 US-08-226-264-7	Sequence 2, Appl
10	68	30.9	14	1 US-08-226-264-19	Sequence 19, Appl
11	68	30.9	16	1 US-08-226-264-8	Sequence 8, Appl
12	68	30.9	16	1 US-08-226-264-21	Sequence 21, Appl
13	67.5	30.7	280	4 US-09-214-095D-119	Sequence 119, Appl
14	66.5	30.2	24	3 US-08-584-031-8	Sequence 8, Appl
15	66.5	30.2	24	3 US-08-780-496-8	Sequence 8, Appl
16	66	30.0	20	1 US-08-416-336-4	Sequence 17, Appl
17	66	30.0	76	3 US-08-956-307B-17	Sequence 17, Appl
18	66	30.0	76	3 US-08-956-307B-18	Sequence 18, Appl
19	66	30.0	122	3 US-08-956-307B-19	Sequence 19, Appl
20	65.5	29.8	17	3 US-09-136-421-10	Sequence 10, Appl
21	65.5	29.8	18	1 US-08-578-649-14	Sequence 14, Appl
22	65.5	29.8	18	1 US-08-670-175-8	Sequence 8, Appl
23	65.5	29.8	29	5 PCT-US94-05150-37	Sequence 37, Appl
24	64.5	29.3	254	3 US-09-167-434-7	Sequence 7, Appl
25	64.5	29.3	254	3 US-08-853-755-7	Sequence 4, Appl
26	64	29.1	211	4 US-08-856-253-4	Sequence 19, Appl
27	62.5	28.4	53	2 US-08-651-818A-19	Sequence 19, Appl

28	62.5	28.4	53	4 US-09-184-826-19	Sequence 19, Appl
29	62.5	28.4	54	2 US-08-651-818A-23	Sequence 23, Appl
30	62.5	28.4	54	4 US-09-184-826-23	Sequence 23, Appl
31	62.5	28.4	335	4 US-09-095-117-2	Sequence 2, Appl
32	62.5	28.4	335	4 US-09-095-117-4	Sequence 4, Appl
33	62	28.2	43	2 US-08-652-818A-43	Sequence 43, Appl
34	62	28.2	68	1 US-08-330-638D-2	Sequence 2, Appl
35	62	28.2	68	2 US-08-906-746A-2	Sequence 2, Appl
36	62	28.2	397	3 US-08-978-741-6	Sequence 6, Appl
37	62	28.2	397	4 US-09-333-729A-7	Sequence 7, Appl
38	62	28.2	492	2 US-08-644-271-32	Sequence 32, Appl
39	61	27.7	10	4 US-09-197-801-14	Sequence 14, Appl
40	61	27.7	10	4 US-09-551-028-14	Sequence 14, Appl
41	61	27.7	10	4 US-09-202-101-17	Sequence 17, Appl
42	61	27.7	301	2 US-08-661-052-14	Sequence 14, Appl
43	61	27.7	301	4 US-09-188-082-14	Sequence 14, Appl
44	61	27.7	391	5 PCT-US95-15696-2	Sequence 2, Appl
45	61	27.7	448	4 US-09-461-474-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-467-155A-7
; Sequence 7, Application US/08467155A
; Patent No. 5736377
; GENERAL INFORMATION:
; APPLICANT: Band, Viola
; TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA, AND RELATED
; NUMBER OF INVENTION: MOLECULES AND METHODS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,155A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00398/100001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-467-155A-7

Query Match 38.2%; Score 84; DB 1; Length 281;
Best local similarity 66.7%; Pred. No. 0.00025;
Matches 18; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 MNLILITFVAAGAAVAFDDDKLVHG 27
DB 1 MSALLITLVAAGAAVAFVDDDKIVGG 27


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:
: TELEFAX: 611/542-8906
:
: TELEX: 200154
:
: INFORMATION FOR SEQ. ID NO: 7:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 281 amino acids
:
: TYPE: amino acid
:
: STRANDEDNESS: not relevant
:
: TOPOLOGY: linear
:
: - MOLECULE TYPE: protein
:
: PCT-US96-07343-7

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Query Match	38.2%;	Score	84;	DB	5;	Length	281;
Best Local Similarity	65.7%;	Pred. No.	0.00025;				
Matches	18;	Conservative	2;	Mismatches	7;	Indels	0;
				Gaps			0

Qy 1 MNLILITFVAANAAPEDDDDKLVHG 27
| : ||| | ||| | |||| : | |
Db 1 MSALLILALVGAAVAFPVDDDDKIVGG 27

RESULT 5
US-08-978-

Sequence 44, Application US/08978404B
Patent No. 5968782
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: FAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINOGEN
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:

STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA

; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE

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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
;

```

```

SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97

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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/032,354

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;
; FILING DATE: 04-DEC-1996
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Plumer, Elizabeth R.
;

REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
517 530 2700

TELEPHONE: 617-720-3333
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR CEO TD NO.:

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; INFORMATION FOR SEQ ID NO: 44
;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 246 amino acids
;   TYPE: amino acid

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LIFE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: NO 5968782a

MOLECULE APT. NO. 3506/022

Query Match	36.8%;	Score 81;	DB 2;	Length 246;
Best Local Similarity	63.0%;	Pred. No. 0.00055;		
Matches 17: Conservative	3;	Mismatches 7;	Indels	

QY 1 MNLILLTFVAAAVAPFDDDDKLVHG 27

Db 1 MSALLILALVGAAVAEPLEDDDKIVGG 27

RESULT 6

US-08-965-762-20
; Sequence 20, Application US/08965762
; Patent No. 6380963

; FALCON NO: 0280503
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Koltin, Yigal
 ; ADDRESSEE: Gaurias, Yigal

APPLICANT: SAVILAS, VICTORIA
TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
FILE REFERENCE: 07334/062001
CURRENT APPLICATION NUMBER: US/08/965 762

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;
; CURRENT AFFILIATION NUMBER: 00/00/2000/100
;
; CURRENT FILING DATE: 1997-11-07
;
; NUMBER OF SEQ ID NOS: 35
;
; SOFTWARE: FastSeq for Windows Version 3.0

```

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; COLNAME: ADDRESS      COORDINATE
; SEQ ID NO 20
; LENGTH: 401
TYPE: PRT

```

ORGANISM: *Saccharomyces cerevisiae*
US-08-965-762-20

Query Match	34.3%	Score 75.5;	DB 4;	Length 401;
Best Local Similarity	39.5%;	Pred. No. 0.0058;		
Matches 15; Conservative	7;	Mismatches 13;	Indels 3;	Gaps 1

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Qy      6  ILTFVAAVAAPRDDDDKLVHGKLIHHNNHHN---DDDDK 400
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      38  VLADANSSIDAPENIKKKKKPKNNHHHHHHSKREGNDK 755
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RESULT 7
US-08-956-267A-2

; Sequence 2, Application US/08956267A
; Patent No. 5945328

```

; GENERAL INFORMATION:
; APPLICANT: WOLDIKE, Helle Fabricius
; APPLICANT: KUJELDSEN, Thomas Borglum

```

```

; TITLE OF INVENTION: A Process For Producing Trypsin
; TITLE OF INVENTION: (Trypsinogen)
; NUMBER OF SEQUENCES: 6

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 59453280 NO. 5945328disk of NO. 5945328th America, Inc
STREET: 405 Lexington Avenue

CITY: New York
STATE: NY
COUNTRY: USA

```

;      ZIP: 101/4
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Diskette
;      GENERATED BY: GENIE 4.2b

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; COMPUTER: IBM compatible
;
; OPERATING SYSTEM: DOS
;
; SOFTWARE: FastSeq for Windows Version 2.0
;
; CURRENT APPLICATION:

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CLASSIFICATION: 433
ATTORNEY/AGENT INFORMATION:
NAME: Rozek, Carol
REGISTRATION NUMBER: 36

REGISTRATION NUMBER: 20,022
REFERENCE/DOCKET NUMBER: 4500.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123

TELEPHONE: 212-878-9655
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:

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LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear

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MOLECULE TYPE: protein
US-08-956-267A-2

Query Match 32.3%; Score 71; DB 2; Length 247;
 Best Local Similarity 53.8%; Pred. No. 0.014;
 Matches 14; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 2 NLLILFVAAVAAPFDDDKLVHG 27
 Db 3 NTFVLLALGAAVAFPTDDDKIVGG 28

RESULT 8

US-08-226-264-7
 ; Sequence 7, Application US/08226264
 ; Patent No. 5801017
 ; GENERAL INFORMATION:
 ; APPLICANT: Werber, Moshe M.
 ; APPLICANT: Zeelon, Elisha P.
 ; APPLICANT: Levanon, Avigdor
 ; APPLICANT: Guy, Rachel
 ; APPLICANT: Goldlust, Arle
 ; APPLICANT: Rigbi, Meir
 ; APPLICANT: Panet, Amos
 ; APPLICANT: Fischer, Meir
 ; TITLE OF INVENTION: PRODUCTION OF RECOMBINANT FACTOR XA
 ; TITLE OF INVENTION: INHIBITORS OF LEECH HIRUDO MEDICINALIS
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/226,264
 ; FILING DATE: 08-APR-94
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 40017-A/JPW/GJG
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-278-0400
 ; TELEFAX: 212-391-0525
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; US-08-226-264-7

Query Match 30.9%; Score 68; DB 1; Length 14;
 Best Local Similarity 78.6%; Pred. No. 0.0012;
 Matches 11; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

OY 29 LHHHHH--DDDK 40
 :||||| |||||
 Db 1 MHHHHHGTDDDK 14

RESULT 9

US-08-226-264-19
 ; Sequence 19, Application US/08226264
 ; Patent No. 5801017
 ; GENERAL INFORMATION:
 ; APPLICANT: Werber, Moshe M.
 ; APPLICANT: Zeelon, Elisha P.
 ; APPLICANT: Levanon, Avigdor
 ; APPLICANT: Guy, Rachel
 ; APPLICANT: Goldlust, Arle
 ; APPLICANT: Rigbi, Meir
 ; APPLICANT: Panet, Amos
 ; APPLICANT: Fischer, Meir
 ; TITLE OF INVENTION: PRODUCTION OF RECOMBINANT FACTOR XA
 ; TITLE OF INVENTION: INHIBITORS OF LEECH HIRUDO MEDICINALIS
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/226,264
 ; FILING DATE: 08-APR-94
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 40017-A/JPW/GJG
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-278-0400
 ; TELEFAX: 212-391-0525
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; US-08-226-264-19

Query Match 30.9%; Score 68; DB 1; Length 14;
 Best Local Similarity 78.6%; Pred. No. 0.0012;
 Matches 11; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

OY 29 LHHHHH--DDDK 40
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 Db 1 MHHHHHGTDDDK 14

RESULT 10

US-08-226-264-20
 ; Sequence 20, Application US/08226264
 ; Patent No. 5801017
 ; GENERAL INFORMATION:
 ; APPLICANT: Werber, Moshe M.
 ; APPLICANT: Zeelon, Elisha P.
 ; APPLICANT: Levanon, Avigdor
 ; APPLICANT: Guy, Rachel
 ; APPLICANT: Goldlust, Arle
 ; APPLICANT: Rigbi, Meir
 ; APPLICANT: Panet, Amos

APPLICANT: Fischer, Meir
TITLE OF INVENTION: PRODUCTION OF RECOMBINANT FACTOR XA
TITLE OF INVENTION: INHIBITORS OF LEECH HIRUDO MEDICINALIS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/226,264
FILING DATE: 08-APR-94
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40017-A/JPW/GJG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-226-264-20

Query Match 30.9%; Score 68; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 0.0012;
Matches 11; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 29 LHHHHH--DDDK 40
DB 1 MHHHHHGTDDDK 14

RESULT 11
US-08-226-264-8
Sequence 8, Application US/08226264
Patent No. 5801017
GENERAL INFORMATION:
APPLICANT: Werber, Moshe M.
APPLICANT: Zeelon, Elisha P.
APPLICANT: Levanon, Avigdor
APPLICANT: Guy, Rachel
APPLICANT: Goldlust, Arle
APPLICANT: Rigbi, Meir
APPLICANT: Fischer, Meir
APPLICANT: Panet, Amos
TITLE OF INVENTION: PRODUCTION OF RECOMBINANT FACTOR XA
TITLE OF INVENTION: INHIBITORS OF LEECH HIRUDO MEDICINALIS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/226,264
FILING DATE: 08-APR-94
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40017-A/JPW/GJG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-226-264-8

Query Match 30.9%; Score 68; DB 1; Length 16;
Best Local Similarity 78.6%; Pred. No. 0.0014;
Matches 11; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 29 LHHHHH--DDDK 40
DB 1 MHHHHHGTDDDK 14

RESULT 12
US-08-226-264-21
Sequence 21, Application US/08226264
Patent No. 5801017
GENERAL INFORMATION:
APPLICANT: Werber, Moshe M.
APPLICANT: Zeelon, Elisha P.
APPLICANT: Levanon, Avigdor
APPLICANT: Guy, Rachel
APPLICANT: Goldlust, Arle
APPLICANT: Rigbi, Meir
APPLICANT: Panet, Amos
APPLICANT: Fischer, Meir
TITLE OF INVENTION: PRODUCTION OF RECOMBINANT FACTOR XA
TITLE OF INVENTION: INHIBITORS OF LEECH HIRUDO MEDICINALIS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/226,264
FILING DATE: 08-APR-94
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.

REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 40017-A/JPW/GJG
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-278-0400
 TELEFAX: 212-391-0525
 TELEX:
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 US-08-226-264-21

Query Match 30.9%; Score 68; DB 1; Length 16;
 Best Local Similarity 78.6%; Pred. No. 0.0014;
 Matches 11; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

OY 29 LHHHHH--DDDDK 40
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 DB 1 MHHHHHGTDDDK 14

RESULT 13
 US-09-214-095D-119
 ; Sequence 119, Application US/09214095D
 ; Patent No. 6280987
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry, Donald
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; FILE REFERENCE: 51400-A-PCT-US
 ; CURRENT APPLICATION NUMBER: US/09/214, 095D
 ; CURRENT FILING DATE: 1999-07-19
 ; NUMBER OF SEQ ID NOS: 121
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 119
 ; LENGTH: 280
 ; TYPE: PRT
 ; ORGANISM: Murine
 US-09-214-095D-119

Query Match 30.7%; Score 67.5; DB 4; Length 280;
 Best Local Similarity 75.0%; Pred. No. 0.05;
 Matches 12; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

OY 19 DDDDKLVHGLHHHH 34
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 DB 268 DDDDKLVH--HHHH 280

RESULT 14
 US-08-584-031-8
 ; Sequence 8, Application US/08584031A
 ; Patent No. 6030945
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; TITLE OF INVENTION: APO-2 LIGAND
 ; FILE REFERENCE: 11669, 22US03
 ; CURRENT APPLICATION NUMBER: US/08/584, 031A
 ; CURRENT FILING DATE: 1996-01-09
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 8
 ; LENGTH: 24
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:

NAME/KEY: UNSURE
 LOCATION: (1)..(24)
 OTHER INFORMATION: Sequence is synthesized
 Patent No. 6030945
 US-08-584-031-8

Query Match 30.2%; Score 66.5; DB 3; Length 24;
 Best Local Similarity 60.0%; Pred. No. 0.0036;
 Matches 12; Conservative 0; Mismatches 3; Indels 5; Gaps 1;

OY 26 HGKLVHHHH--DDDDK 40
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 DB 3 HHHHHHHHSSGHIDDDK 22

RESULT 15
 US-08-780-496-8
 ; Sequence 8, Application US/08780496
 ; Patent No. 6046048
 ; GENERAL INFORMATION:
 ; APPLICANT: Avi Ashkenazi, Anan Chuntcharapai, Kyung Jin Kim
 ; TITLE OF INVENTION: APO-2 Ligand
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/780,496
 FILING DATE: 08-Jan-1997
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Marschang, Diane L.
 REGISTRATION NUMBER: 35,600
 REFERENCE/DOCKET NUMBER: P0978P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-5416
 TELEFAX: 415/952-9881

TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 amino acids
 TYPE: Amino Acid
 TOPOLOGY: linear
 US-08-780-496-8

Query Match 30.2%; Score 66.5; DB 3; Length 24;
 Best Local Similarity 60.0%; Pred. No. 0.0036;
 Matches 12; Conservative 0; Mismatches 3; Indels 5; Gaps 1;

OY 26 HGKLVHHHH--DDDDK 40
 :||||| |||||
 DB 3 HHHHHHHHSSGHIDDDK 22

Search completed: March 15, 2002, 06:44:18
 Job time: 1072 sec

Fri Mar 15 06:40:14 2002

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Page 7

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